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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/538,396DATE: 04/19/2000
TIME: 17:20:17

Input Set: I538396.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Mahajan, Pramod B.
 2 Shi, Jinrui
 3 <120> TITLE OF INVENTION: Maize Rad50 Orthologue and Uses Thereof
 4 <130> FILE REFERENCE: 1116
 5 <140> CURRENT APPLICATION NUMBER: US/09/538,396
 6 <141> CURRENT FILING DATE: 2000-03-29
 7 <150> EARLIER APPLICATION NUMBER: 60/132,575
 8 <151> EARLIER FILING DATE: 1999-05-05
 9 <160> NUMBER OF SEQ ID NOS: 3
 10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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 12 <211> LENGTH: 4492
 13 <212> TYPE: DNA
 14 <213> ORGANISM: Zea mays
 15 <220> FEATURE:
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 21 ctccactgcc cctccttttc tctttccaaat cgttttgcaa tcactacgag cgtaatgaat 180
 22 agaagttgat agggagatag catccgcaat ctaggtttgg ggcaatcgct ctggccagac 240
 23 tggateggag tgcaagtgcgt agagggaggc acttggggct cgtggggcaa g atg agc 297
 24 Met Ser
 25 1
 26 acc gtt gac aag atg ctg atc aag ggg att cgg agc ttc gat ccg gac 345
 27 Thr Val Asp Lys Met Leu Ile Lys Gly Ile Arg Ser Phe Asp Pro Asp
 28 5 10 15
 29 aat aag aac gtc atc acc ttc ttc aag ccg ctc acc ctc atc gtt ggc 393
 30 Asn Lys Asn Val Ile Thr Phe Phe Lys Pro Leu Thr Leu Ile Val Gly
 31 20 25 30
 32 ccc aac ggt gct ggc aag acc acg atc atc gag tgc ctg aag ctt tct 441
 33 Pro Asn Gly Ala Gly Lys Thr Thr Ile Ile Glu Cys Leu Lys Leu Ser
 34 35 40 45 50
 35 tgc acc ggc gag ctg ccc ccc aac tcc cgc tct ggc cac acc ttc gtc 489
 36 Cys Thr Gly Glu Leu Pro Pro Asn Ser Arg Ser Gly His Thr Phe Val
 37 55 60 65
 38 cac gac ccc aag gta gct ggc gag acg gaa aca aaa gga caa att aag 537
 39 His Asp Pro Lys Val Ala Gly Glu Thr Glu Thr Lys Gly Gln Ile Lys
 40 70 75 80
 41 ttg cgg ttt aag act gca gca gga aag gat gtg gtg tgc atc cgg tcc 585
 42 Leu Arg Phe Lys Thr Ala Ala Gly Lys Asp Val Val Cys Ile Arg Ser
 43 85 90 95
 44 ttc cag ctt acc caa aag gca tca aag atg gag ttt aag gca att gaa 633

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48	Ser Val Leu Gln Thr Ile Asn Pro His Thr Gly Glu Lys Val Cys Leu	
49	115 120 125 130	
50	agc tac aga tgt gct gac atg gat aga gag att cct gcc tta atg ggt	729
51	Ser Tyr Arg Cys Ala Asp Met Asp Arg Glu Ile Pro Ala Leu Met Gly	
52	135 140 145	
53	gtt tcg aag gcc gta ctg gag aat gtt ata ttt gtt cac caa gat gaa	777
54	Val Ser Lys Ala Val Leu Glu Asn Val Ile Phe Val His Gln Asp Glu	
55	150 155 160	
56	tcc aat tgg cca ttg cag gac ccg tca aca ctt aag aag aag ttc gat	825
57	Ser Asn Trp Pro Leu Gln Asp Pro Ser Thr Leu Lys Lys Phe Asp	
58	165 170 175	
59	gac atc ttc tct gcc aca cgc tat acg aaa gct ctt gaa gtc ata aag	873
60	Asp Ile Phe Ser Ala Thr Arg Tyr Thr Lys Ala Leu Glu Val Ile Lys	
61	180 185 190	
62	aaa ctt cac aag gat caa atg caa gag atc aag act ttt agg tta aag	921
63	Lys Leu His Lys Asp Gln Met Gln Glu Ile Lys Thr Phe Arg Leu Lys	
64	195 200 205 210	
65	ctg gag aac ctt cag act gta aaa gac caa gca cat aag ctg cgt gaa	969
66	Leu Glu Asn Leu Gln Thr Val Lys Asp Gln Ala His Lys Leu Arg Glu	
67	215 220 225	
68	aat att gct caa gat caa gaa aag tca gat gcc tca aaa tct cag atg	1017
69	Asn Ile Ala Gln Asp Gln Glu Lys Ser Asp Ala Ser Lys Ser Gln Met	
70	230 235 240	
71	gag caa ctg aag gaa aag atc tgt ggt acc gag aga gaa atc ctg caa	1065
72	Glu Gln Leu Lys Glu Lys Ile Cys Gly Thr Glu Arg Glu Ile Leu Gln	
73	245 250 255	
74	atg gaa aca agt ttg gat gaa ctg aga aga ctt cag gga caa att gac	1113
75	Met Glu Thr Ser Leu Asp Glu Leu Arg Arg Leu Gln Gly Gln Ile Asp	
76	260 265 270	
77	atc aag gca aca gag aga agt aca tta ctt acg cag cag cat gaa aag	1161
78	Ile Lys Ala Thr Glu Arg Ser Thr Leu Leu Thr Gln Gln His Glu Lys	
79	275 280 285 290	
80	ctt gct gca ctt tct gag gaa aat gaa gat acc gat gag gaa cta atg	1209
81	Leu Ala Ala Leu Ser Glu Glu Asn Glu Asp Thr Asp Glu Glu Leu Met	
82	295 300 305	
83	gaa tgg caa aca aaa ttt gaa gaa agg att gcg tta cta gaa aca aaa	1257
84	Glu Trp Gln Thr Lys Phe Glu Glu Arg Ile Ala Leu Leu Glu Thr Lys	
85	310 315 320	
86	atc agt aaa ctt gta aga gat atg gat gat gaa gca tct tat agc tcc	1305
87	Ile Ser Lys Leu Val Arg Asp Met Asp Asp Glu Ala Ser Tyr Ser Ser	
88	325 330 335	
89	gtt ctg tcc aaa caa aat tct gaa tta aca cat gaa att gga aag ctc	1353
90	Val Leu Ser Lys Gln Asn Ser Glu Leu Thr His Glu Ile Gly Lys Leu	
91	340 345 350	
92	cag gca gaa gct gat gct cac ctg act atg aag cat gaa cga gac tca	1401
93	Gln Ala Glu Ala Asp Ala His Leu Thr Met Lys His Glu Arg Asp Ser	
94	355 360 365 370	

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95	gac ata aaa aat ata tgc act aaa cat aat ctt ggg ccg gtt cct gaa	1449
96	Asp Ile Lys Asn Ile Cys Thr Lys His Asn Leu Gly Pro Val Pro Glu	
97	375 380 385	
98	cat ccc ttt acg aat gat gtt gct atg aac ctt aca aac agg att aaa	1497
99	His Pro Phe Thr Asn Asp Val Ala Met Asn Leu Thr Asn Arg Ile Lys	
100	390 395 400	
101	gcg aga cta tca agt ctt gag aat gat ttg ctg gat aag aag aaa tcc	1545
102	Ala Arg Leu Ser Ser Leu Glu Asn Asp Leu Leu Asp Lys Lys Ser	
103	405 410 415	
104	aat gaa gat cag tta gat gtt ttg tgg aaa cac tat ctt aaa ata aat	1593
105	Asn Glu Asp Gln Leu Asp Val Leu Trp Lys His Tyr Leu Lys Ile Asn	
106	420 425 430	
107	gct cgc tac tcc gaa gtt gat ggt cag ata caa tct aag att gaa tcc	1641
108	Ala Arg Tyr Ser Glu Val Asp Gly Gln Ile Gln Ser Lys Ile Glu Ser	
109	435 440 445 450	
110	atg tca ggc att tta aga cgg aga aaa gat aaa gag aaa gaa cgc gat	1689
111	Met Ser Gly Ile Leu Arg Arg Lys Asp Lys Glu Lys Glu Arg Asp	
112	455 460 465	
113	gct gca gaa gtg gag ctt tca aaa ttt aat cta tcc cgt atc gat gag	1737
114	Ala Ala Glu Val Glu Leu Ser Lys Phe Asn Leu Ser Arg Ile Asp Glu	
115	470 475 480	
116	agg gag aga cat atg caa att gaa gtc gag agg aag aca ctt gcg ctt	1785
117	Arg Glu Arg His Met Gln Ile Glu Val Glu Arg Lys Thr Leu Ala Leu	
118	485 490 495	
119	gga gaa aga gac tat gat tca att ata agt cag aaa cga aca gaa gta	1833
120	Gly Glu Arg Asp Tyr Asp Ser Ile Ile Ser Gln Lys Arg Thr Glu Val	
121	500 505 510	
122	tat agt ttg gaa cag aaa ata aaa gtg ctt ctg cgg gag aaa gat ata	1881
123	Tyr Ser Leu Glu Gln Lys Ile Lys Val Leu Leu Arg Glu Lys Asp Ile	
124	515 520 525 530	
125	ata aat aga aat gct gat gaa aga gta aaa ctg ggt ttg aag aag gat	1929
126	Ile Asn Arg Asn Ala Asp Glu Arg Val Lys Leu Gly Leu Lys Lys Asp	
127	535 540 545	
128	gca ttg gaa agc agc aag gac aag ctc aat gag ata gtt aat gag cat	1977
129	Ala Leu Glu Ser Ser Lys Asp Lys Leu Asn Glu Ile Val Asn Glu His	
130	550 555 560	
131	aag gat aaa atc aaa aag gta ctt agg ggg agg aat cct ttt gag aag	2025
132	Lys Asp Lys Ile Lys Lys Val Leu Arg Gly Arg Asn Pro Phe Glu Lys	
133	565 570 575	
134	gat atg aag aag gag atc aat caa gcc ttt tgg cct gtg gac aag gaa	2073
135	Asp Met Lys Lys Glu Ile Asn Gln Ala Phe Trp Pro Val Asp Lys Glu	
136	580 585 590	
137	tac aat gag tta aga tca aaa tcc cag gaa gca gag caa gag ctt aaa	2121
138	Tyr Asn Glu Leu Arg Ser Lys Ser Gln Glu Ala Glu Gln Glu Leu Lys	
139	595 600 605 610	
140	ttt act cag agc aaa gta act gat gct aga gaa caa ttg aca aaa ctt	2169
141	Phe Thr Gln Ser Lys Val Thr Asp Ala Arg Glu Gln Leu Thr Lys Leu	
142	615 620 625	
143	cga aga gat atg gat gca aaa aga aga ttc ctg gac tcg aaa ctt caa	2217
144	Arg Arg Asp Met Asp Ala Lys Arg Arg Phe Leu Asp Ser Lys Leu Gln	

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145	630	635	640	
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147	Ser Ile Leu Gln Ile Ser Ala Asn Val Asp Met Phe Pro Lys Val Leu			
148	645	650	655	
149	caa gac gcc atg aac aaa aga gat gaa cag aaa aga tta gag aat ttc			2313
150	Gln Asp Ala Met Asn Lys Arg Asp Glu Gln Lys Arg Leu Glu Asn Phe			
151	660	665	670	
152	gca aat gga atg cgg gaa atg ctt gca cct ttt gaa cat ttg gct cgg			2361
153	Ala Asn Gly Met Arg Glu Met Leu Ala Pro Phe Glu His Leu Ala Arg			
154	675	680	685	690
155	aag aat cat gta tgc cca tgc tgt gaa cgt gct ttc aca cct gat gag			2409
156	Lys Asn His Val Cys Pro Cys Glu Arg Ala Phe Thr Pro Asp Glu			
157	695	700	705	
158	gag gat gag ttc gtg aag aaa caa agg atg caa aac tca agt act gca			2457
159	Glu Asp Glu Phe Val Lys Lys Gln Arg Met Gln Asn Ser Ser Thr Ala			
160	710	715	720	
161	gag aga tct aaa gct ctg gca atg gaa tca tca aat gct gaa gct ctt			2505
162	Glu Arg Ser Lys Ala Leu Ala Met Glu Ser Ser Asn Ala Glu Ala Leu			
163	725	730	735	
164	ttt cag caa ttg gat aaa ctt cgg act atc tat gat gct tat gtg aag			2553
165	Phe Gln Gln Leu Asp Lys Leu Arg Thr Ile Tyr Asp Ala Tyr Val Lys			
166	740	745	750	
167	ctg gta gaa gaa acc ata cct cta gca gag aaa aac ttg aat caa cat			2601
168	Leu Val Glu Glu Thr Ile Pro Leu Ala Glu Lys Asn Leu Asn Gln His			
169	755	760	765	770
170	ttg gcg gat gaa agt cag aag gcg cag gca ttt gat gat ctt ttg ggt			2649
171	Leu Ala Asp Glu Ser Gln Lys Ala Gln Ala Phe Asp Asp Leu Leu Gly			
172	775	780	785	
173	gtt ctt gcc cat gtt caa atg gac agg gat gca gtg gaa gcc tta tta			2697
174	Val Leu Ala His Val Gln Met Asp Arg Asp Ala Val Glu Ala Leu Leu			
175	790	795	800	
176	caa ccc act gat act att gac agg cat gta cat gaa att caa cag cta			2745
177	Gln Pro Thr Asp Thr Ile Asp Arg His Val His Glu Ile Gln Gln Leu			
178	805	810	815	
179	gtc aaa gaa gta gaa gat ctt gaa tat gca ctt gat tct agt ggc cga			2793
180	Val Lys Glu Val Glu Asp Leu Glu Tyr Ala Leu Asp Ser Ser Gly Arg			
181	820	825	830	
182	ggt gtc aag tct ttg gag gaa att caa ctg gag ctg aac ttt ctg cag			2841
183	Gly Val Lys Ser Leu Glu Glu Ile Gln Leu Glu Leu Asn Phe Leu Gln			
184	835	840	845	850
185	aga aca agg gac aca ttg att gtc gaa gtg gat gat ctt aga gat caa			2889
186	Arg Thr Arg Asp Thr Leu Ile Val Glu Val Asp Asp Leu Arg Asp Gln			
187	855	860	865	
188	cat aga atg cta aat gaa gat atg tca agt gct cag gtg aga tgg cac			2937
189	His Arg Met Leu Asn Glu Asp Met Ser Ser Ala Gln Val Arg Trp His			
190	870	875	880	
191	aat gct cgg gaa gag aaa gtg aaa gct tct agc ata ttg gaa aga ttc			2985
192	Asn Ala Arg Glu Glu Lys Val Lys Ala Ser Ser Ile Leu Glu Arg Phe			
193	885	890	895	
194	caa aaa tct gaa gag gaa ttg gtg ctt cta gct gag gaa aaa gaa caa			3033

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195	Gln	Lys	Ser	Glu	Glu	Glu	Leu	Val	Leu	Leu	Ala	Glu	Glu	Gln			
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197	ctg	att	gta	gaa	aag	aag	ctt	tta	gaa	gag	tct	ctt	gat	cca	ttg	tcc	3081
198	Leu	Ile	Val	Glu	Lys	Lys	Leu	Leu	Glu	Glu	Ser	Leu	Asp	Pro	Leu	Ser	
199	915			920			925			930							
200	aaa	gag	aaa	gag	agc	ttg	ttg	caa	gag	tat	aat	gct	ttg	aag	caa	aag	3129
201	Lys	Glu	Glu	Ser	Leu	Leu	Gln	Glu	Tyr	Asn	Ala	Leu	Lys	Gln	Lys		
202	935			940			945										
203	ctg	gat	gaa	gag	tat	cat	cag	ctt	gca	gaa	aga	aaa	agg	gag	ttc	cag	3177
204	Leu	Asp	Glu	Glu	Tyr	His	Gln	Leu	Ala	Glu	Arg	Lys	Arg	Glu	Phe	Gln	
205	950			955			960										
206	caa	gaa	ctt	gat	gct	ctt	gga	aga	ctt	aat	atg	aag	ata	aaa	ggg	tac	3225
207	Gln	Glu	Leu	Asp	Ala	Leu	Gly	Arg	Leu	Asn	Met	Lys	Ile	Lys	Gly	Tyr	
208	965			970			975										
209	ttg	gat	tcc	aag	aaa	aac	gaa	aag	ctt	aag	gaa	ttg	cag	gga	agg	cat	3273
210	Leu	Asp	Ser	Lys	Lys	Asn	Glu	Lys	Leu	Lys	Glu	Leu	Gln	Gly	Arg	His	
211	980			985			990										
212	gtt	ctt	tgc	cat	tct	cag	tta	cag	agt	tgc	atg	gca	aaa	cag	caa	aga	3321
213	Val	Leu	Cys	His	Ser	Gln	Leu	Gln	Ser	Cys	Met	Ala	Lys	Gln	Gln	Arg	
214	995			1000			1005			1010							
215	ata	tca	gct	gag	tta	aac	aag	agc	aaa	gaa	cta	ctg	cag	ggc	cag	ggc	3369
216	Ile	Ser	Ala	Glu	Leu	Asn	Lys	Ser	Lys	Glu	Leu	Leu	Gln	Gly	Gln	Gly	
217	1015			1020			1025										
218	cag	ttg	aaa	aga	aac	att	gat	gac	aat	ctc	aag	tac	agg	aaa	aca	aag	3417
219	Gln	Leu	Lys	Arg	Asn	Ile	Asp	Asp	Asn	Leu	Lys	Tyr	Arg	Lys	Thr	Lys	
220	1030			1035			1040										
221	gct	gtg	gaa	caa	ctt	act	cgt	gat	ata	gaa	tca	ctt	gaa	gaa	agg		3465
222	Ala	Asp	Val	Glu	Gln	Leu	Thr	Arg	Asp	Ile	Glu	Ser	Leu	Glu	Arg		
223	1045			1050			1055										
224	ctg	ctt	tca	ata	ggt	agc	ttg	tct	gct	ata	gaa	gct	gat	ctg	aaa	cgc	3513
225	Leu	Leu	Ser	Ile	Gly	Ser	Leu	Ser	Ala	Ile	Glu	Ala	Asp	Leu	Lys	Arg	
226	1060			1065			1070										
227	cat	tct	caa	gaa	aaa	gag	agg	ctt	aat	tca	gaa	ttt	aac	agg	tgg	caa	3561
228	His	Ser	Gln	Glu	Lys	Glu	Arg	Leu	Asn	Ser	Glu	Phe	Asn	Arg	Trp	Gln	
229	1075			1080			1085			1090							
230	gga	aca	ctt	tct	gtt	tat	caa	agt	aat	att	tca	aag	cac	aaa	caa	gag	3609
231	Gly	Thr	Leu	Ser	Val	Tyr	Gln	Ser	Asn	Ile	Ser	Lys	His	Gln	Glu		
232	1095			1100			1105										
233	ctt	aaa	ctg	tca	cag	tac	aag	gat	atc	gag	aag	cga	tat	act	aat	caa	3657
234	Leu	Lys	Leu	Ser	Gln	Tyr	Lys	Asp	Ile	Glu	Lys	Arg	Tyr	Thr	Asn	Gln	
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237	Phe	Leu	Gln	Leu	Lys	Thr	Thr	Glu	Met	Ala	Asn	Lys	Asp	Leu	Asp	Arg	
238	1125			1130			1135										
239	tat	tat	act	gct	tta	gac	aag	gct	ctt	atg	cgg	ttc	cac	agc	atg	aag	3753
240	Tyr	Tyr	Ala	Leu	Asp	Lys	Ala	Leu	Met	Arg	Phe	His	Ser	Met	Lys		
241	1140			1145			1150										
242	atg	gag	gag	ata	aat	aaa	ata	atc	aag	gaa	ctg	tgg	caa	cag	aca	tac	3801
243	Met	Glu	Glu	Ile	Asn	Lys	Ile	Ile	Lys	Glu	Leu	Trp	Gln	Gln	Thr	Tyr	
244	1155			1160			1165			1170							

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**VERIFICATION SUMMARY
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Line ? Error/Warning

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